

Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: ____)

```

1 GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61 ACTGCACAAC CACCAGTGAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCACAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTTCCTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTTA GGCAATTTTG CTGTTGGCTC TGATTTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTTTCC TAGATAGAAG ATTAGTTCAT TTGGTTCATT TTGTCTTTGA
361 AGCAAGCCAA GCTCATGAGC CAGTTGGTTA TTTGTCATAA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC

```

Figure 2A. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.

```

1 gccggcctccagcagcgggcgcggcgggcgcgagcagcagcccccactctcctgcgggccgcg
61 ggtggagcagcgcgagccccgcctcgctgagccggccggggcgaggatgagttgcgcc
121 cccgcggcagcgcggccaggatggggagggagcgcgaggcactgcctcgagaactggcgct
181 ccggtgaagtaggcgcgcggcgcgctccgcctcccccagccgttccgcaccgcggccgc
1      M A G S G A W K R L K S M L R K
241 tcagcctctgccATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17 D D A P L F L N D T S A F D F S D E A G
301 GATGATGCGCCGCTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGGCGGGG
37 D E G L S R F N K L R V V V A D D G S E
361 GACGAGGGGCTTTCTCGGTTCAACAAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAA
57 A P E R P V N G A H P T L Q A D D D S L
421 GCCCCGAAAGGCCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTA
77 L D Q D L P L T N S Q L S L K V D S C D
481 CTGGACCAAGACTTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGAC
97 N C S K Q R E I L K Q R K V K A R L T I
541 AACTGCAGCAAACAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117 A A V L Y L L F M I G E L V G G Y I A N
601 GCTGCCGTTCTGTACTTGCTTTTCATGATTGGAGAAGTTGTAGGTGGATACATTGCAAAT
137 S L A I M T D A L H M L T D L S A I I L
661 AGCCTAGCAATCATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTC
157 T L L A L W L S S K S P T K R F T F G F
721 ACCCTGCTTGCTTTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTT
177 H R L E V L S A M I S V L L V Y I L M G

```

781 CATCGCTTAGAGGTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGA
 197 F L L Y E A V Q R T I H M N Y E I N G D
 841 TTCCTCTTATATGAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGAT
 217 I M L I T A A V G V A V N V I M G F L L
 901 ATAATGCTCATCACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTG
 237 N Q S G H R H S H S H S L P S N S P T R
 961 AACCAGTCTGGTCACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATCCCCCTACCAGA
 257 G S G C E R N H G Q D S L A V R A A F V
 1021 GGTTCCTGGGTGTGAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTA
 277 H A L G D L V Q S V G V L I A A Y I I R
 1081 CATGCTTTGGGAGATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGA
 297 F K P E Y K I A D P I C T Y V F S L L V
 1141 TTCAAGCCAGAATACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG
 317 A F T T F R I I W D T V V I I L E G V P
 1201 GCTTTTACAACATTTTGAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCA
 337 S H L N V D Y I K E A L M K I E D V Y S
 1261 AGCCATTTGAATGTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCA
 357 V E D L N I W S L T S G K S T A I V H I
 1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTTCACATA
 377 Q L I P G S S S K W E E V Q S K A N H L
 1381 CAGCTAATTCCTGGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTA
 397 L L N T F G M Y R C T I Q L Q S Y R Q E
 1441 TTATTGAACACATTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAA
 417 V D R T C A N C Q S S S P *
 1501 GTGGACAGAACTTGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttgggaa
 1561 ctctctgccttatttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatga
 1621 gaaaatggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccc
 1681 cagcctgacagtgctagtctctgtttaatggtaaaaggagactttgccataattttcaga
 1741 tgaagatgtttcccaaactgtttacagaatgagatgtgactctacagatacctcatag
 1801 aagacaatccaagatcatacttcattaacttgacagagtagctgtcttaaaggaagcatc
 1861 aagaattcaatattttgcatttaaaaaatactttttaaggccattttatattaagccagtgc
 1921 tggaaaactgaattttttttattatgtataataatctcgacacccagcttctggaattgc
 1981 tgcttttctttttacagaaattactaccaacagatttcaggaagtactagtagttatccc
 2041 aaaagtggaataagcatgtattcctaagtgtttcagaaatgttttatttcacacataagt
 2101 cttaatgtttattgtttatgattatactttataaacaaccttttccagatgctacagggttt
 2161 tgaatctcaaagttaacattttttcattattttgtaatcttagaaccaaatctttattttatt
 2221 gtggctcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag

2281 ttagtcttaaaactcaaattactatatgatgatttaaacaataaaagagcgaggatgg
2341 ggaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 108P5H8 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```

1  M A G S G A W K R L K S M L R K D D A P
1  ATGGCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTAAATGACACCAGCGCCTTTGACTTCTCGGATGAGCGGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGGAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTAACTGACCTAAGCGCCATCATACTCACCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAAGATTCACCTTTGGATTTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCCCTCCCTGCCTTCAAATCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N

```

961 TTTCGAATCATATGGGATACAGTAGTTATAATACTAGAAAGGTGTGCCAAGCCATTTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTCAGCTTCAGAGTTACAGGCAAGAAGTGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattttggggactcctgccttat
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaaatggaatc
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt
1441 gctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaagatgtttc
1501 ccaaactgtttacagaatgagatgtgactctacagatacctcatag

Figure 2C. The cDNA (SEQ ID. NO. :____) and amino acid sequence (SEQ ID. NO. :____) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

```

1 M A G S G A W K R L K S M L R K D D A P
1 ATGGCCCGGCTCTGGCGCGTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F E F S D E A G D E G L
61 CTGTTTTTTAAATGACACCAGCGCCTTTGAGTTCTCGGATGAGGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAACGGGGCGCACCCGACCCTCCAGGCCGACGATGATTCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTCACCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATTTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAAGAACTATCCATATGAACTATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGCAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACCAGTCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATTCCTCCCTGCTTCAAATTCCTTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATCTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATCATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTGGCTTTTACAACA

```

321 F R I I W D T V V I I L E G V P S H L N
961 TTTCTGAATCATATGGGATACAGTAGTTATAATACTAGAAAGGTGTGCCAAGCCATTTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAAttttatgtattgttttagcattgctgaatt
1321 cactttatttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaa
1381 atggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagc
1441 ctgacagtgctagtctctgtttaatggtaaaaggagactttgccataattttcagatgaa
1501 gatgtttcccaaactgttttacagaatgagatgtgactcctacagatacctcatag

Figure 3:

Figure 3A. Amino acid sequence corresponding to 108P5H8 v.1 and 108P5H8 v.2 (SEQ ID. NO. : ____). The 108P5H8 v.1 and 108P5H8 v.2 proteins have 429 amino acids.

```

1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFD  FSDEAGDEGL  SRFNKL RVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSL LDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQRKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILLTLLA  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVA VNV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAF TT  FRIIWDTVVI  ILEGVP SHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGMYRCTIQL  QSYRQEV DRT
421 CANCQSSSP*

```

Figure 3B. Amino acid sequence corresponding to 108P5H8 v.3 (SEQ ID. NO. : ____).

The 108P5H8 v.3 protein has 429 amino acids.

```

1  MAGSGAWKRL  KSMRLRKDDAP  LFLNDTSAFE  FSDEAGDEGL  SRFNKL RVVV  ADDGSEAPER
61  PVNGAHPTLQ  ADDDSL LDQD  LPLTNSQLSL  KVDSCDNCSK  QREILKQRKV  KARLTIAAVL
121 YLLFMIGELV  GGYIANSLAI  MTDALHMLTD  LSAILLTLLA  LWLSSKSPTK  RFTFGFHRLE
181 VLSAMISVLL  VYILMGFLLY  EAVQRTIHMN  YEINGDIMLI  TAAVGVA VNV  IMGFLLNQSG
241 HRHSHSHSLP  SNSPTRGSGC  ERNHGQDSL A  VRAAFVHALG  DLVQSVGVLI  AAYIIRFKPE
301 YKIADPICTY  VFSLLVAF TT  FRIIWDTVVI  ILEGVP SHLN  VDYIKEALMK  IEDVYSVEDL
361 NIWSLTSGKS  TAIVHIQLIP  GSSSKWEEVQ  SKANHLLLNT  FGMYRCTIQL  QSYRQEV DRT
421 CANCQSSSP*

```


Figure 4:

Figure 4A Nucleic acid sequence alignment of the 3 variants of 108P5H8. Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

	1	15	16	30	31	45	46	60	61	75	76	
90												
	v.1	GCCGGCCTCCAGCAG	CGGGCGGGCGGGGCG	CGAGCACGACCCAC	TCTCCTGCGGCCGCG	GGTGGAGCAGCGCGA						
		GCCCGCCTCGCTGAG										
	v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
	v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	
180		91	105	106	120	121	135	136	150	151	165	166
	v.1	CCGGCCGGGGCGGG	GAGATGAGTTGCGGC	CCCGCGGCAGCGCCC	CAGGATGGGGAGGGA	CGCGCGGCACTGCCCC						
		TCGAGAACTGGCGCT										
	v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
	v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
270		181	195	196	210	211	225	226	240	241	255	256
	v.1	CCGGTGAAGTAGGCG	CCGCCGGCCGTCCGC	CTCCCCAAGCCGTT	CCGCACCGCGGCCGC	TCAGCCTCTGCCATG						
		GCCGGCTCTGGCGCG										
	v.2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
	v.3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
		-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
		GCCGGCTCTGGCGCG										
		GCCGGCTCTGGCGCG										

360 271 285 286 300 301 315 316 330 331 345 346
v.1 TGAAGCGCCTCAAA TCTATGCTAAGGAAG GATGATGCGCCGCTG TTTTAAATGACACC AGCGCCTTTGACTTC
TCGGATGAGCGCGGG
v.2 TGAAGCGCCTCAAA TCTATGCTAAGGAAG GATGATGCGCCGCTG TTTTAAATGACACC AGCGCCTTTGACTTC
TCGGATGAGCGCGGG
v.3 TGAAGCGCCTCAAA TCTATGCTAAGGAAG GATGATGCGCCGCTG TTTTAAATGACACC AGCGCCTTTGAGGTTC
TCGGATGAGCGCGGG
450 361 375 376 390 391 405 406 420 421 435 436
v.1 GACGAGGGGCTTTCT CGGTTCAACAAACTT CGAGTTGTGTGGCC GATGACGGTTCCGAA GCCCGGAAAGGCCT
GTTAACGGGCGGCAC
v.2 GACGAGGGGCTTTCT CGGTTCAACAAACTT CGAGTTGTGTGGCC GATGACGGTTCCGAA GCCCGGAAAGGCCT
GTTAACGGGCGGCAC
v.3 GACGAGGGGCTTTCT CGGTTCAACAAACTT CGAGTTGTGTGGCC GATGACGGTTCCGAA GCCCGGAAAGGCCT
GTTAACGGGCGGCAC
540 451 465 466 480 481 495 496 510 511 525 526
v.1 CCGACCCCTCCAGGCC GACGATGATTCCCTTA CTGGACCAAGACTTA CCTTTGACCAACAGT CAGCTGAGTTTGAAG
GTGGACTCCTGTGAC
v.2 CCGACCCCTCCAGGCC GACGATGATTCCCTTA CTGGACCAAGACTTA CCTTTGACCAACAGT CAGCTGAGTTTGAAG
GTGGACTCCTGTGAC
v.3 CCGACCCCTCCAGGCC GACGATGATTCCCTTA CTGGACCAAGACTTA CCTTTGACCAACAGT CAGCTGAGTTTGAAG
GTGGACTCCTGTGAC
630 541 555 556 570 571 585 586 600 601 615 616
v.1 AACTGCAGCAAAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGTTGACCATT GCTGCCGTTCTGTAC
TTGCTTTTCAATGATT

v.2 AACTGCAGCAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCAAT GCTGCCGTTCTGTAC
TTGCTTTTCATGATT

v.3 AACTGCAGCAACAG AGAGAGATACTGAAG CAGAGAAAGGTGAAA GCCAGGTTGACCAAT GCTGCCGTTCTGTAC
TTGCTTTTCATGATT

631 645 646 660 661 675 676 690 691 705 706

720

v.1 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCTA
AGCGCCATCATACTC

v.2 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCTA
AGCGCCATCATACTC

v.3 GGAGAACTTGTAGGT GGATACATTGCAAAAT AGCCTAGCAATCATG ACAGATGCACCTTCAT ATGTTAACTGACCTA
AGCGCCATCATACTC

721 735 736 750 751 765 766 780 781 795 796

810

v.1 ACCCTGCTTGCTTTG TGGCTATCATCAAAA TCACCAACC AAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT
TTGTCAGCTATGATT

v.2 ACCCTGCTTGCTTTG TGGCTATCATCAAAA TCACCAACC AAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT
TTGTCAGCTATGATT

v.3 ACCCTGCTTGCTTTG TGGCTATCATCAAAA TCACCAACC AAAAGA TTCACCTTTGGATT CATCGCTTAGAGGTT
TTGTCAGCTATGATT

811 825 826 840 841 855 856 870 871 885 886

900

v.1 AGTGTGCTGTTGGTG TATATACTTATGGGA TTCTCTTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACTAT
GAAATAAATGGAGAT

v.2 AGTGTGCTGTTGGTG TATATACTTATGGGA TTCTCTTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACTAT
GAAATAAATGGAGAT

v.3 AGTGTGCTGTTGGTG TATATACTTATGGGA TTCTCTTTATATGAA GCTGTGCAAAAGAACT ATCCATATGAACTAT
GAAATAAATGGAGAT

[illegible]

v.2 ATCTGTACATACGTA TTTTCATTACTTGTG GCCTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA
CTAGAAAGGTGTGCCA

CTAGAAAGGTGTGCCA
v.3 ATCTGTACATACGTA TTTTCATTACTTGTG GCCTTTTACAACATTT CGAATCATATGGGAT ACAGTAGTTATAATA
CTAGAAAGGTGTGCCA

1261	1275	1276	1290	1291	1305	1306	1320	1321	1335
1336	1350								

1336
v. 1 AGCCATTGAATGTA GACTATATCAAAGAA GCCTTGATGAAAATA GAAGATGTATATTC A GTCCAAGATTTAAAT
1338
ATCTGGTCTCTCACT

ATCTGGTCTCTCACT
v. 2 AGCCATTTGAATGTA GACTATATCAAAGAA GCCTTGATGAAAATA GAAGATGTATATTCA GTCGAAGATTTAAAT
ATCTGGTCTCTCACT

ATCTGGTCTCTCACT
 v. 3 AGCCATTGAATGA GACTATATCAAGAA GCCTTGATGAAAATA GAAGATGTATATTCA GTCGAAGATTTAAAT
 ATCTGGTCTCTCACT

1426	1351	1365	1380	1395	1410	1425
	1440	1366	1381	1396	1411	1425

1428 1440
v.1 TCAGGAAATCTACT GCCATAGTTCACATA CAGCTAATTCCTGGA AGTTCATCTAAATGG GAGGAAGTACAGTCC
AAAGCAACCATTTA

AAAGCAAAACCAATTTA
v.2 TCAGGAAATCTACT GCCATAGTTCACATA CAGCTAATTCTCTGGA AGTTCATCTAAATGG GAGGAAAGTACAGTCC
AAAGCAAAACCAATTTA

AAAGCAAAACCACTTTA
v.3 TCAGGAAATCTACT GCCATAGTTCACATA CAGCTAATTCTGTGA AGTTCATCTAAATGG GAGGAAGTACAGTCC
AAAGCAAAACCATTTA

1441	1455	1456	1470	1471	1485	1486	1500	1501	1515
1516									
1516	1530								

1516
v.1 TTATTGAACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT
1530
GCAAAATTGTCAGAGT

GCCTAATGGTCAGAGT
v.2 TTATTGAACATTT GGCATGTATAGATGT ACTATTGAGCTTCAG AGTTACAGGCAAGAA GTGGACAGAACTTGT
GCTAATGGTCAGAGT

GC AAA T T G T C A G A G T
v.3 T T A T T G A A C A C A T T T G C A T G T A T A G A T G T A C T A T T C A G C T T C A G A G T T A C A G G C A A G A A G T G G A C A G A A C T T G T
G C A A A T T G T C A G A G T

1606 1531 1545 1546 1560 1561 1575 1576 1590 1591 1605
 1620
 v.1 TCTAGTCCCTAAATTT TATGTATT--TTGGG AACTCCTG-----C CTTATTATTATCCTGCA GTCACAGACTTGAGA
 GCAATAAATGCAAAC
 v.2 TCTAGTCCCTAAATTT TATGTATT--TTGGG GACTCCTG-----C CTTATTATTATCCTGCA GTCACAGACTTGAGA
 GCAATAAATGCAAAC
 v.3 TCTAGTCCCTAAATTT TATGTATTGTTTTAG CATTGCTGAATTCAC TTTATTATTATCCTGCA GTCACAGACTTGAGA
 GCAATAAATGCAAAC

1696 1621 1635 1636 1650 1651 1665 1666 1680 1681 1695
 1710
 v.1 CTAAATGAGAAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCAGCCTG
 ACAGTGCTAGTCTCT
 v.2 CTAAATGAGAAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCAGCCTG
 ACAGTGCTAGTCTCT
 v.3 CTAAATGAGAAAAATG GAATCCCTGACAGCT GTGTCCGTATCAAGC ATCAGTCTCTCAAAC AGTTGCCCCAGCCTG
 ACAGTGCTAGTCTCT

1786 1711 1725 1726 1740 1741 1755 1756 1770 1771 1785
 1800
 v.1 GTTTAAATGGTAAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCCAAACACTG TTTACAGAAATGAGAT
 GTGACTC-TACAGAT
 v.2 GTTTAAATGGTAAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCCAAACACTG TTTACAGAAATGAGAT
 GTGACTC-TACAGAT
 v.3 GTTTAAATGGTAAAAG GAGACTTTGCCATAA TTTTCAGATGAAGAT GTTTCCCAAACACTG TTTACAGAAATGAGAT
 GTGACTCCTACAGAT

1876 1801 1815 1816 1830 1831 1845 1846 1860 1861 1875
 1890
 v.1 ACCTCATAGAAGACA ATCCAAGATCATACT TCATTAACTTGACAG AGTACGTGTCTTAAA GGAAGCATCAAGAAT
 TCAATATTGCATTT

v.2 ACCTCATAG-----

v.3 ACCTCATAG-----

1966 1891 1905 1906 1920 1921 1935 1936 1950 1951 1965
1980
v.1 AAAAATACTTTTAA GGCCATTTTATATTA AGCCAGTGTGGAAA ACTGAATTTTTTTA TTATGTATAATAATC
TCGACACCCAGCTTC
v.2 -----

v.3 -----

2056 1981 1995 1996 2010 2011 2025 2026 2040 2041 2055
2070
v.1 TGGAATTGCTGCTTT CTTTTTACAGAAATT ACTACCCAACAGATT TCAGGAAGTACTAGT AGTTATCCCAAAAGT
GGAATAAGCATGTAT
v.2 -----

v.3 -----

2146 2071 2085 2086 2100 2101 2115 2116 2130 2131 2145
2160
v.1 TCCTAAGTGTTTCAG AAATGTTTTTATTCA CACATAAGTCTTAAT GTTATTGTTATGATT ATACTTTATAAACAA
CCTTTTCCAGATGCT
v.2 -----

v.3 -----

2161 2175 2176 2190 2191 2205 2206 2220 2221 2235 2236
2250
v.1 ACAGGGTTTGAATC TCAAAGTTAACATTT TTCAATTATTGTAAT CTTAGAACCAAAATCT TTATTATTGTGGTC
ACTGTTATTAAATGA
v.2 -----

v.3 -----

2251 2265 2266 2280 2281 2295 2296 2310 2311 2325
2326 2340
v.1 TTAGGAAATACTTT CAATATTATTCTGAA TGGCTGAAGTTAGTC TTAAACTCAAATTAC TATATGATGATTAA
AACAAAAATAAAAGAG
v.2 -----

v.3 -----

2341 2355 2356 2370
v.1 CGAGGATGGGAAAA AAAAAAAAAAAAAAAA AAA 2364
v.2 ----- 1548
v.3 ----- 1557

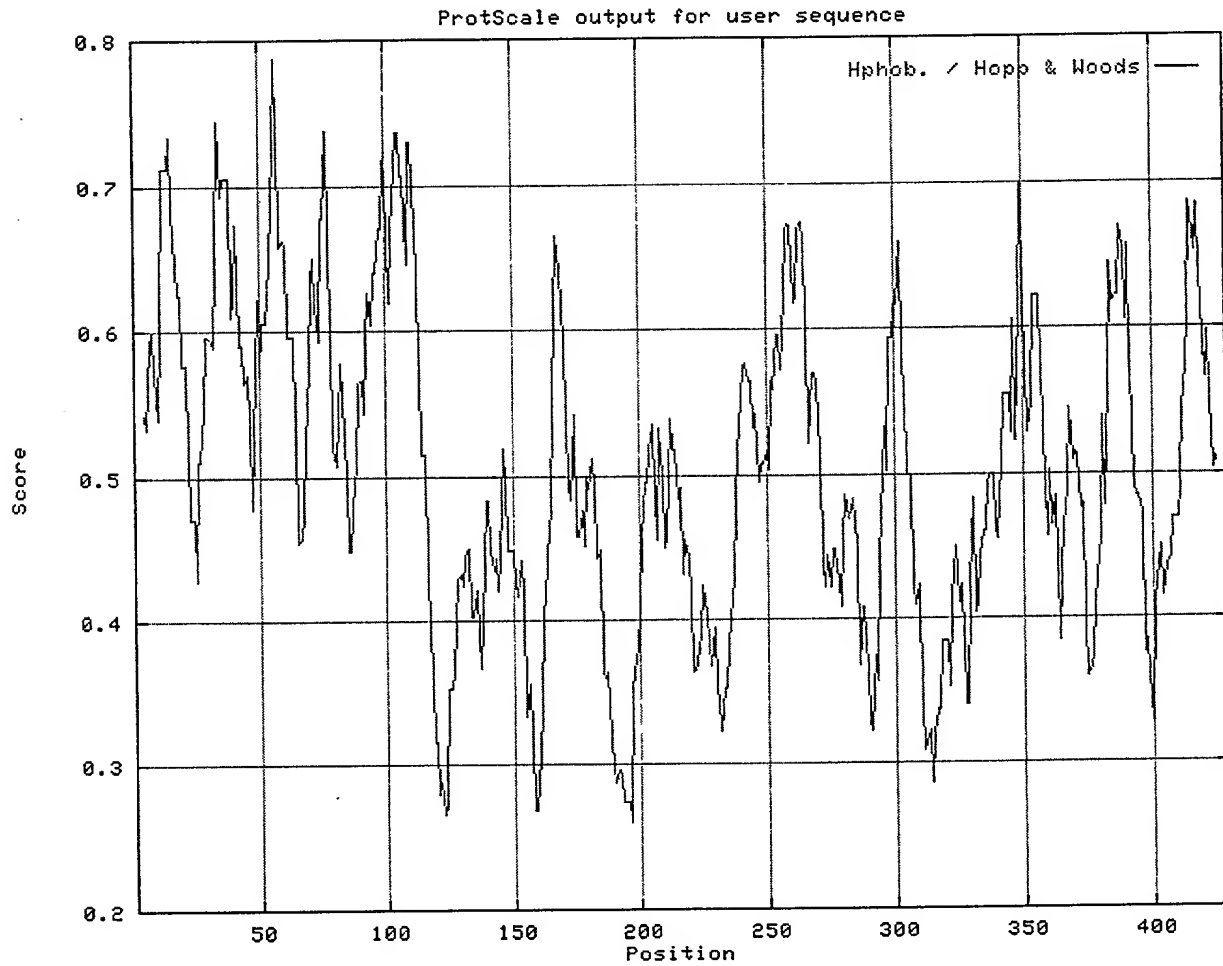
Figure 4B Amino Acid Alignment of the 3 variants of 108P5H8

[illegible]

v.1	VRAAFVHALGDLVQS	GVGLIAAYIIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVPSHLNVDYIK
EALMKIEDVYSVEDL					
v.2	VRAAFVHALGDLVQS	GVGLIAAYIIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVPSHLNVDYIK
EALMKIEDVYSVEDL					
v.3	VRAAFVHALGDLVQS	GVGLIAAYIIIRFKPE	YKIADPICTYVFSLL	VAFTTFRIIWDTVVI	ILEGVPSHLNVDYIK
EALMKIEDVYSVEDL					

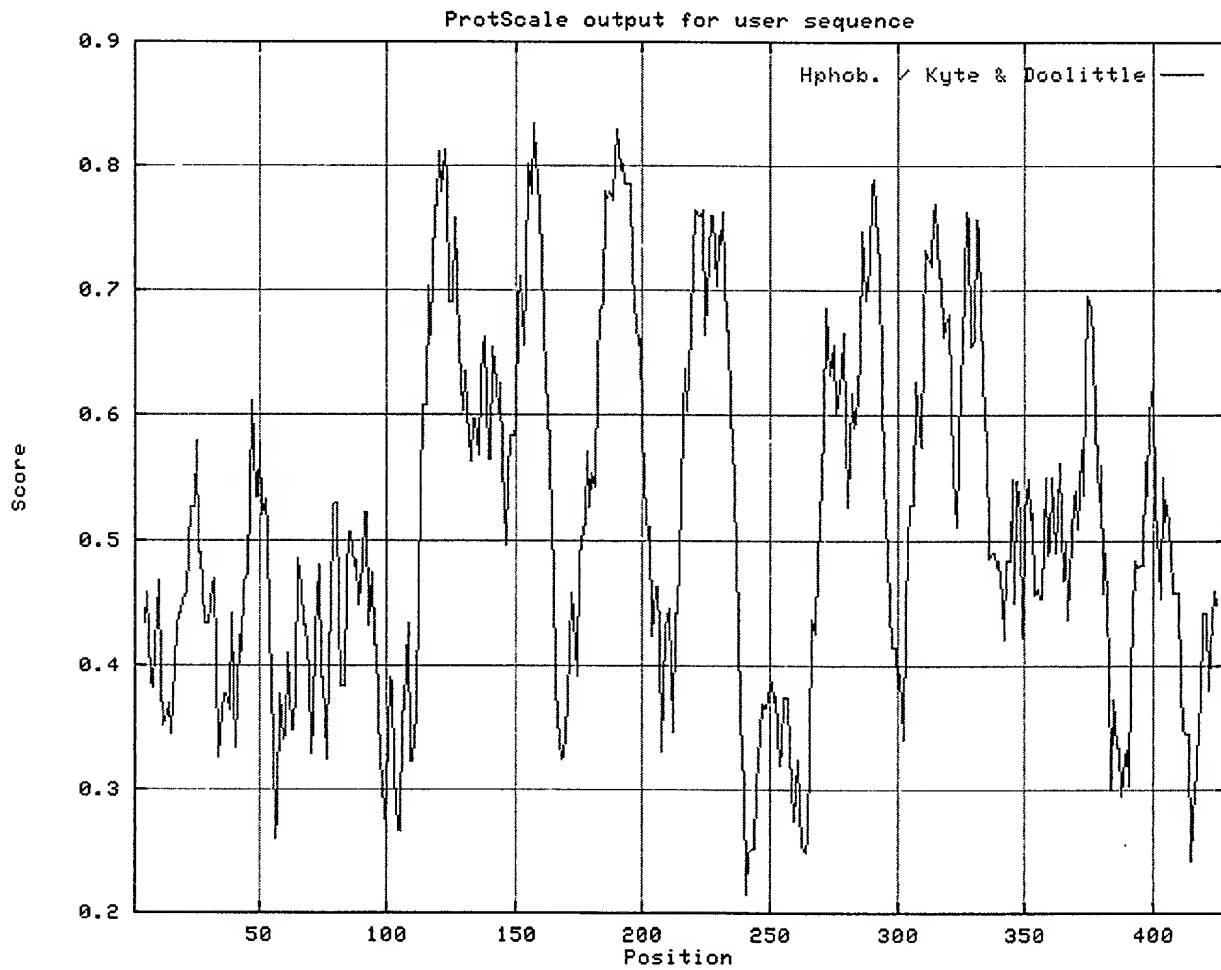
	361	375	376	390	391	405	406	420	421
v. 1	NIWSLTSGKSTAIVH	IQLIPGSSSKWEEVQ	IQLIPGSSSKWEEVQ	SKANHLLLNFTFGMYR	SKANHLLLNFTFGMYR	CTIQLQSYRQEVDR	CTIQLQSYRQEVDR	CANCQSSSP	CANCQSSSP
v. 2	NIWSLTSGKSTAIVH	IQLIPGSSSKWEEVQ	IQLIPGSSSKWEEVQ	SKANHLLLNFTFGMYR	SKANHLLLNFTFGMYR	CTIQLQSYRQEVDR	CTIQLQSYRQEVDR	CANCQSSSP	CANCQSSSP
v. 3	NIWSLTSGKSTAIVH	IQLIPGSSSKWEEVQ	IQLIPGSSSKWEEVQ	SKANHLLLNFTFGMYR	SKANHLLLNFTFGMYR	CTIQLQSYRQEVDR	CTIQLQSYRQEVDR	CANCQSSSP	CANCQSSSP

Figure 5: 108P5H8 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)



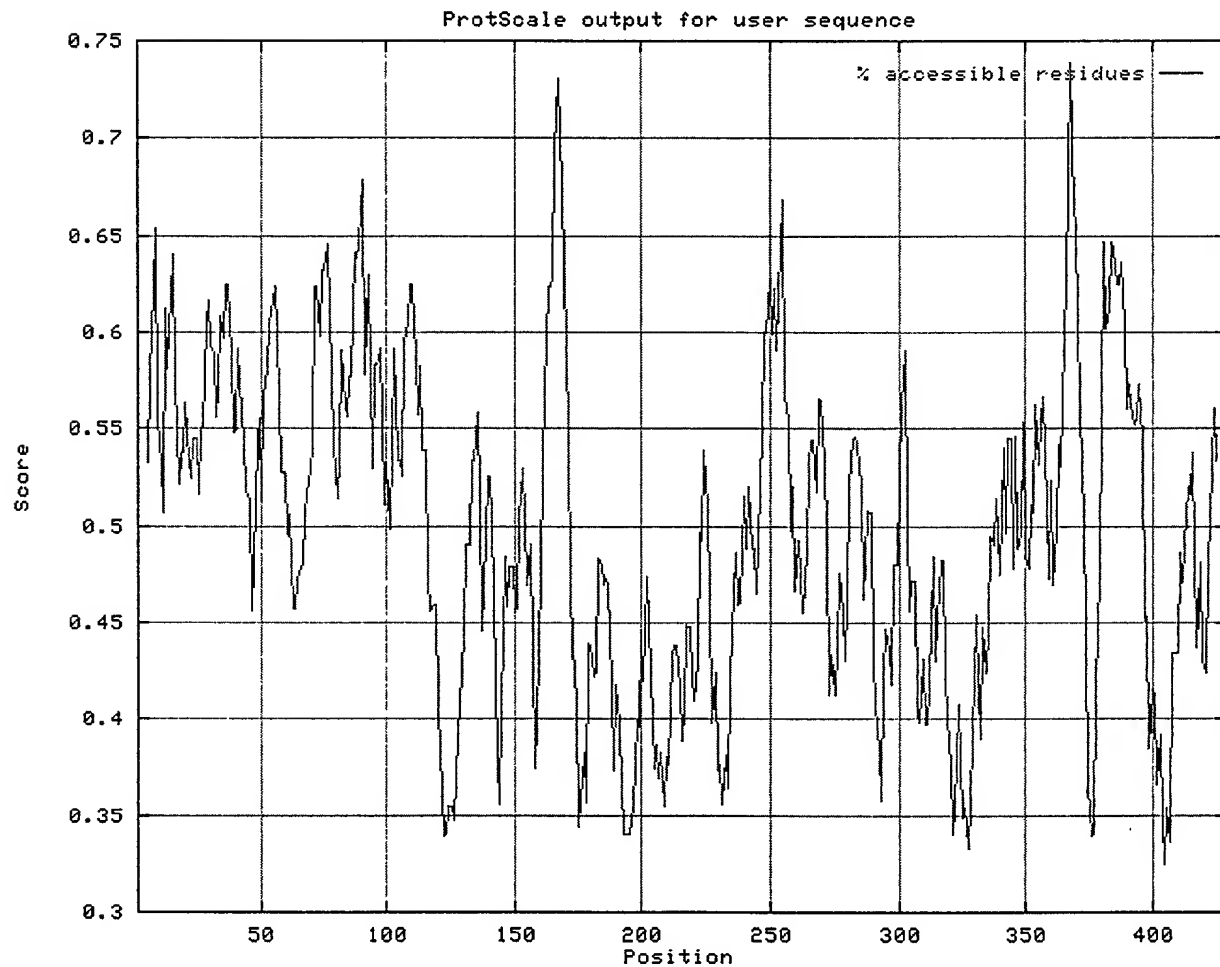
sd-70959

Figure 6: 108P5H8 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)



sd-70959

Figure 7: 108P5H8 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

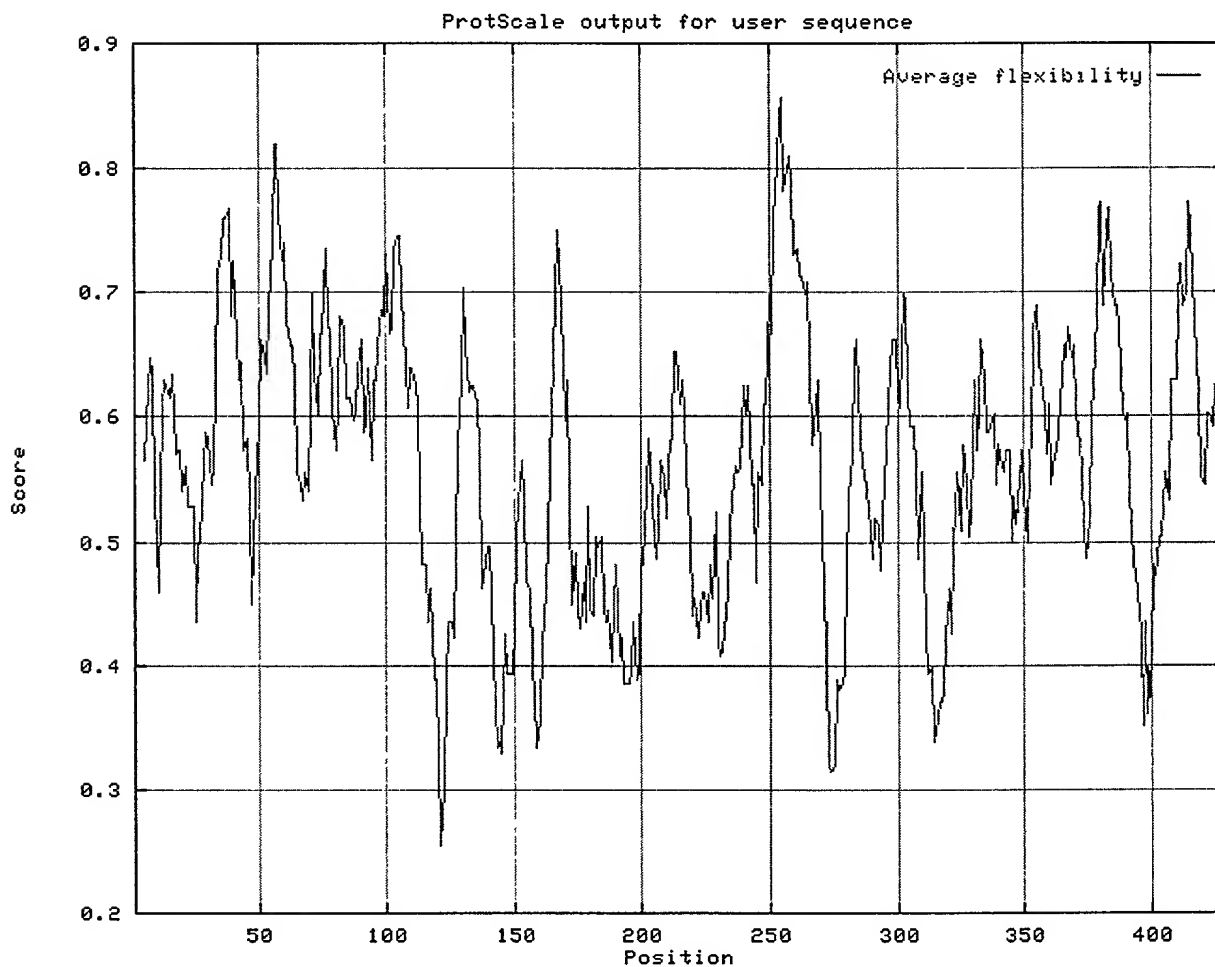


sd-70959

Figure 8: 108P5H8 Average Flexibility Profile

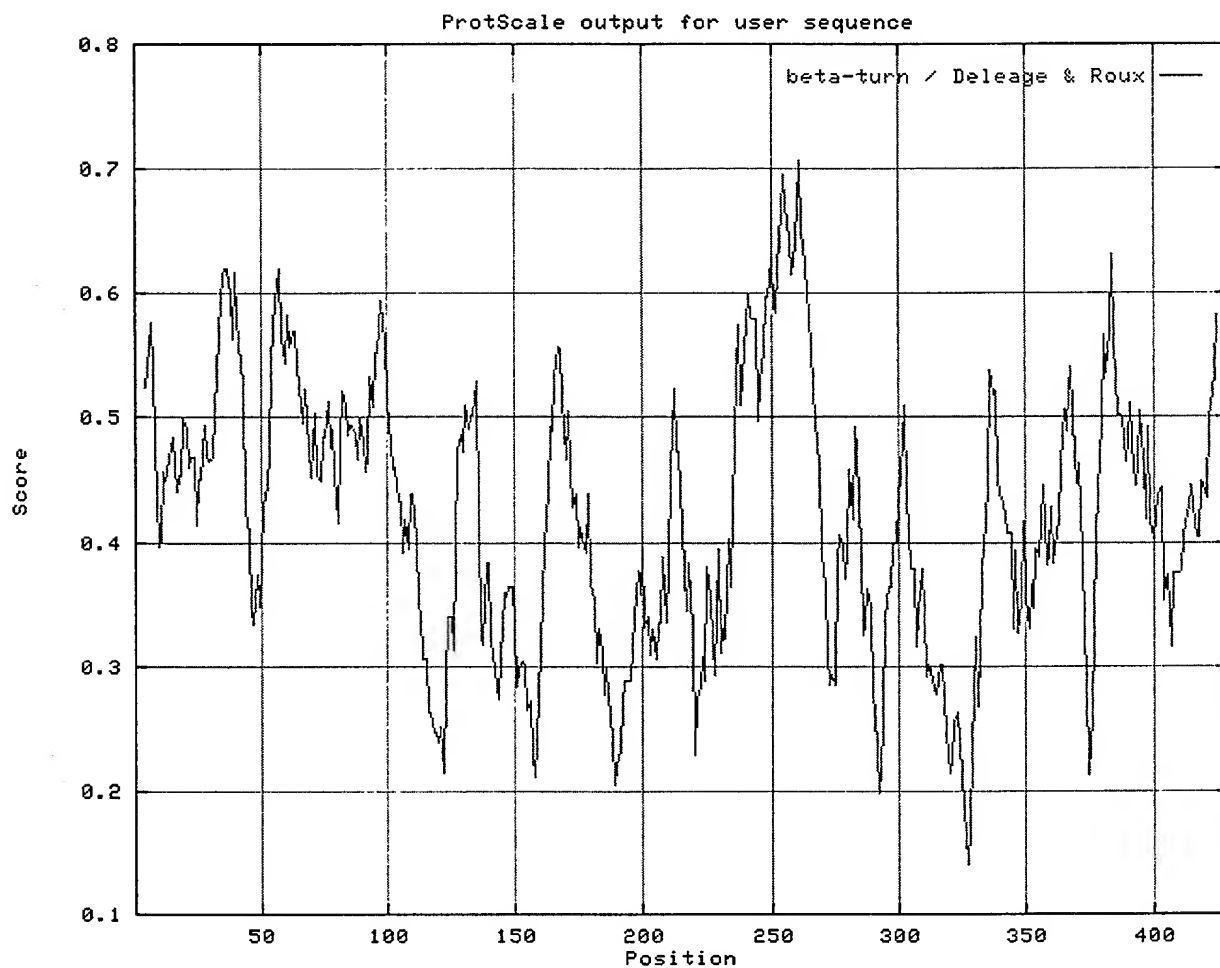
(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)



sd-70959

Figure 9: 108P5H8 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)



sd-70959

Figure 10 Expression of 108P5H8 by RT-PCR

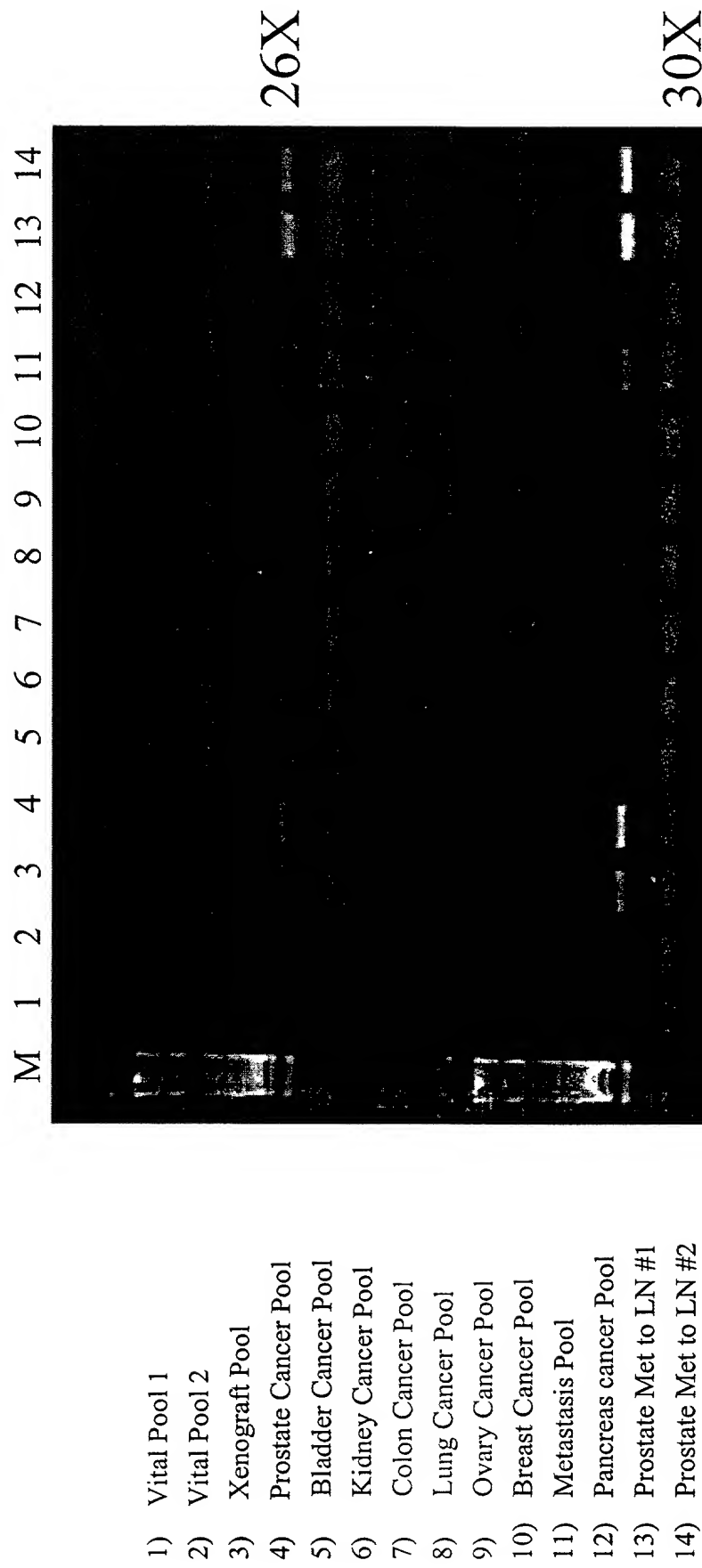


Figure 11 Expression of 108P5H8 in Prostate Cancer Xenografts and restricted normal tissues

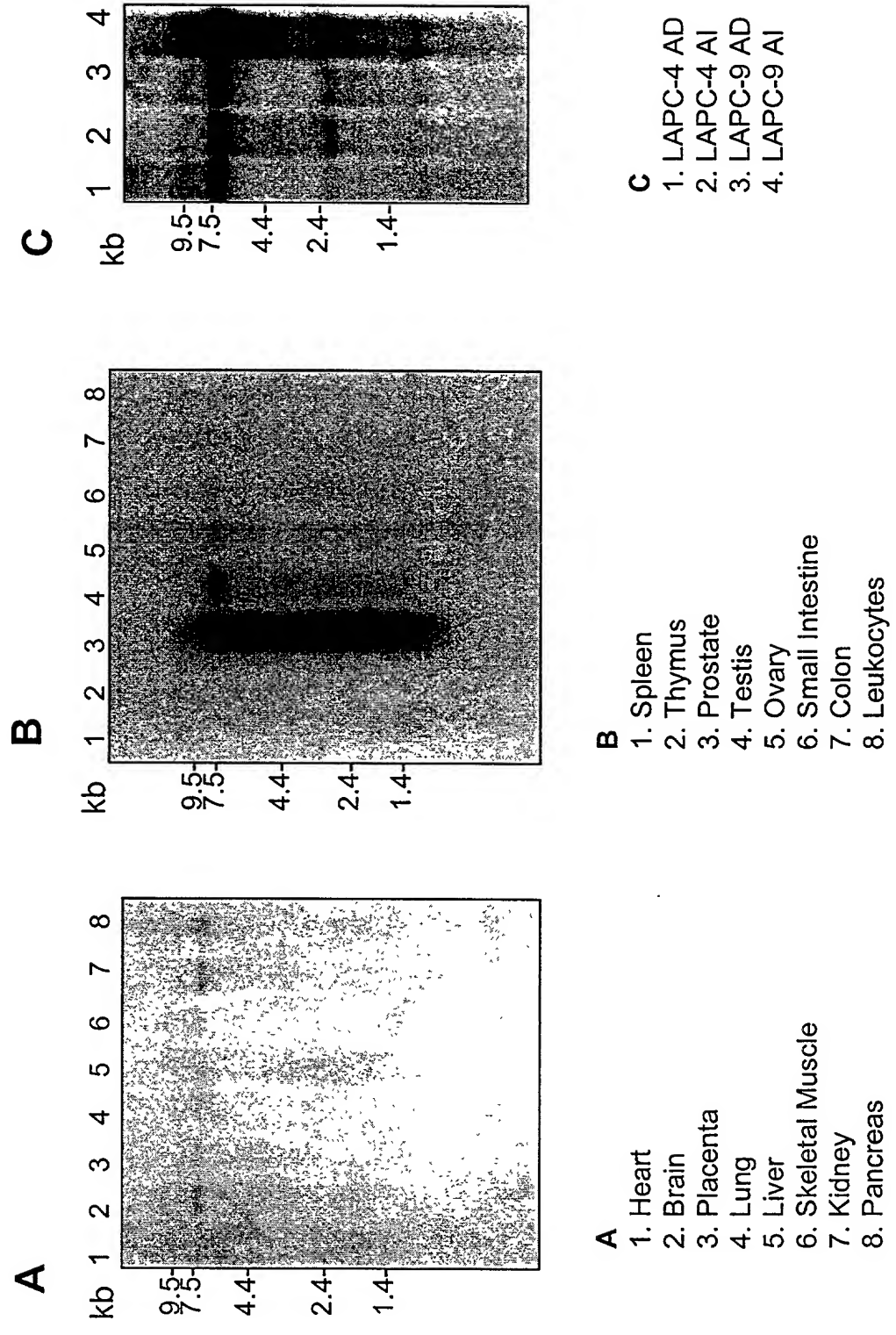


Figure 12 Expression of 108P5H8 in prostate cancer xenografts

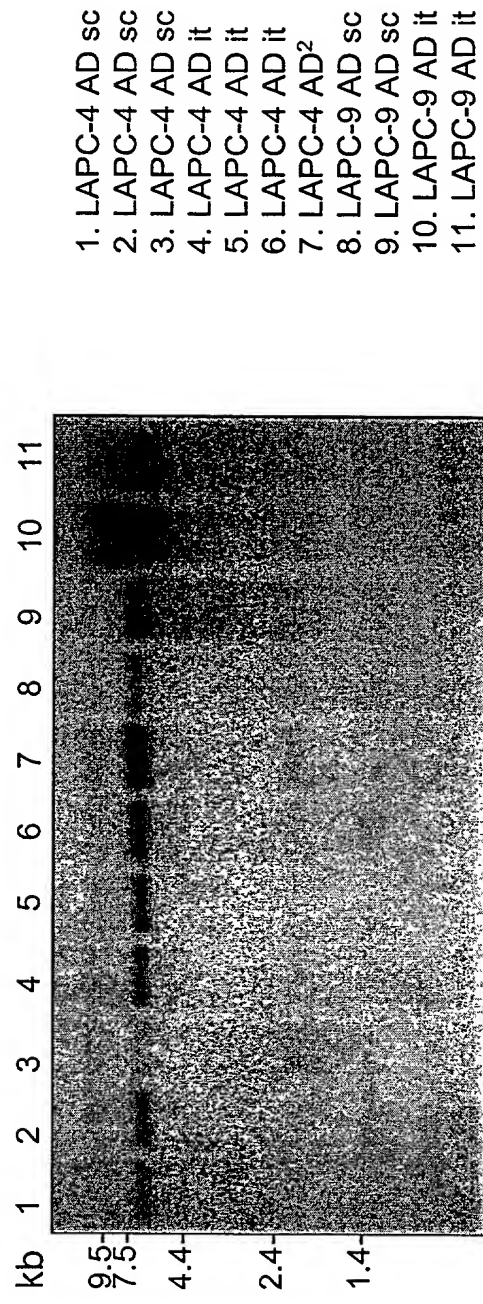


Figure 13 Expression of 108P5H8/ZnT4 in prostate and multiple cancer cell lines

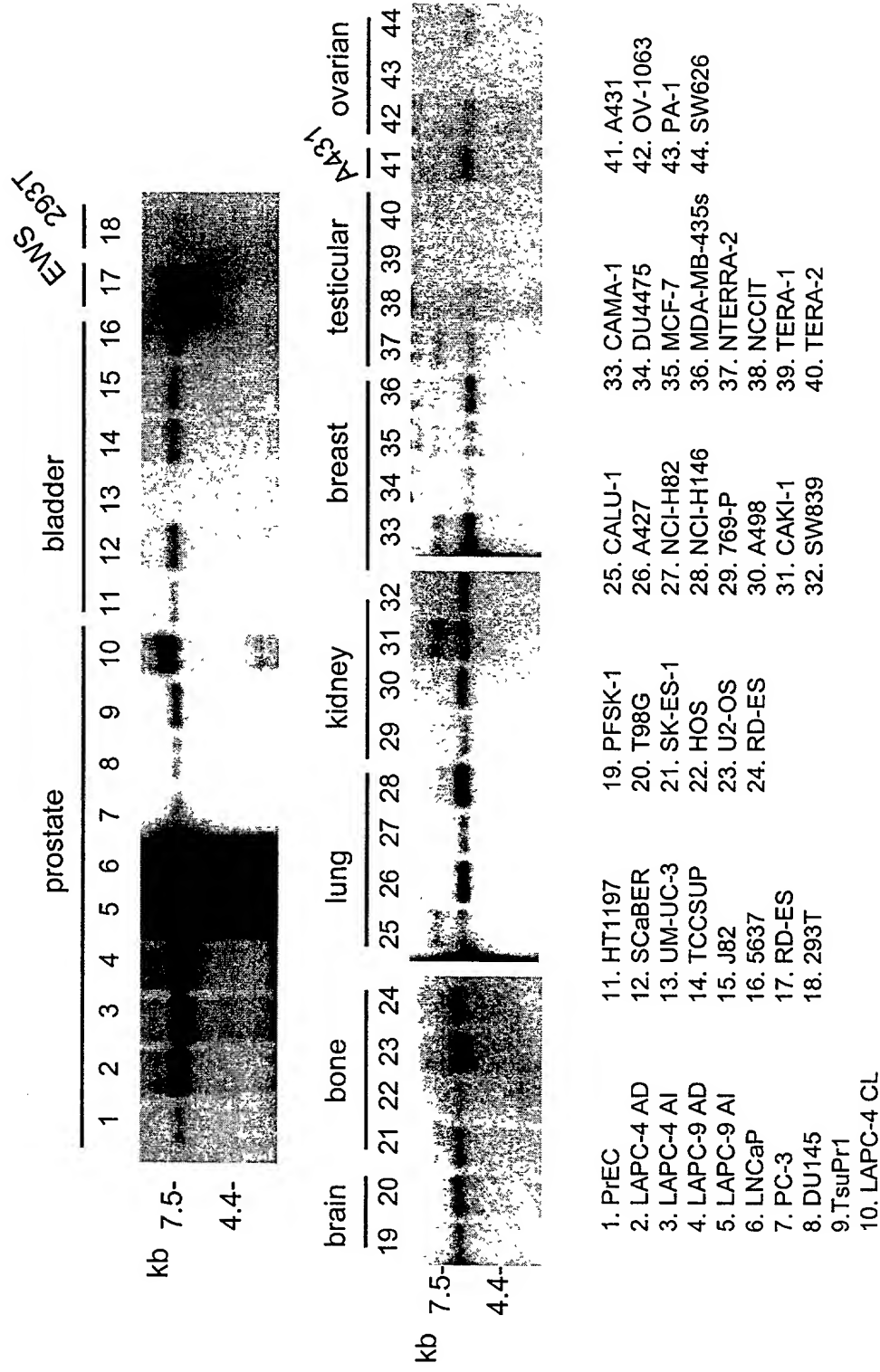


Figure 14 Expression of 108P5H8 in Human Cancers

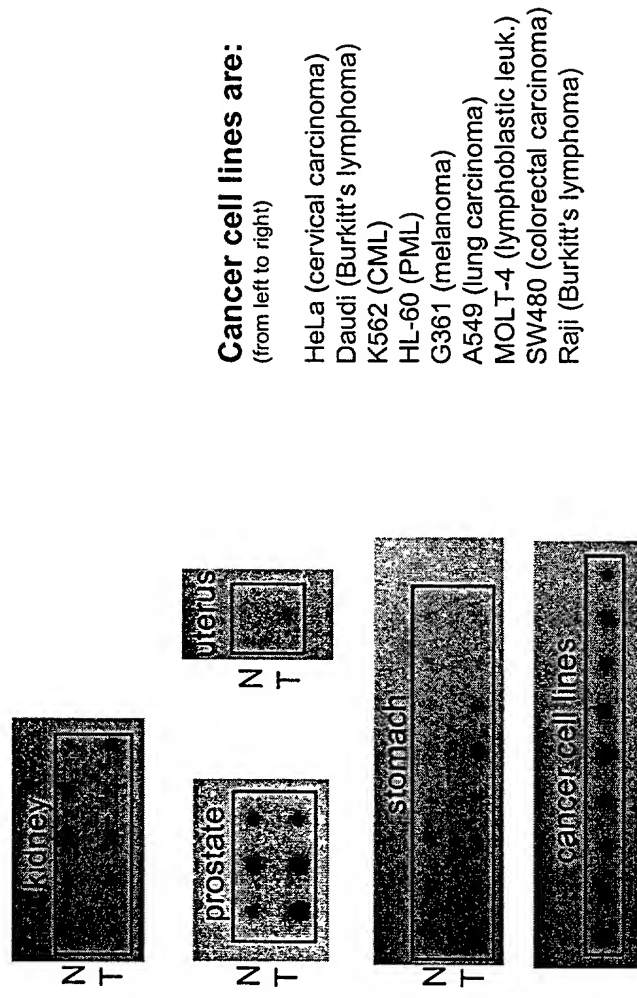


Figure 15 Expression of 108P5H8 in prostate cancer patients samples

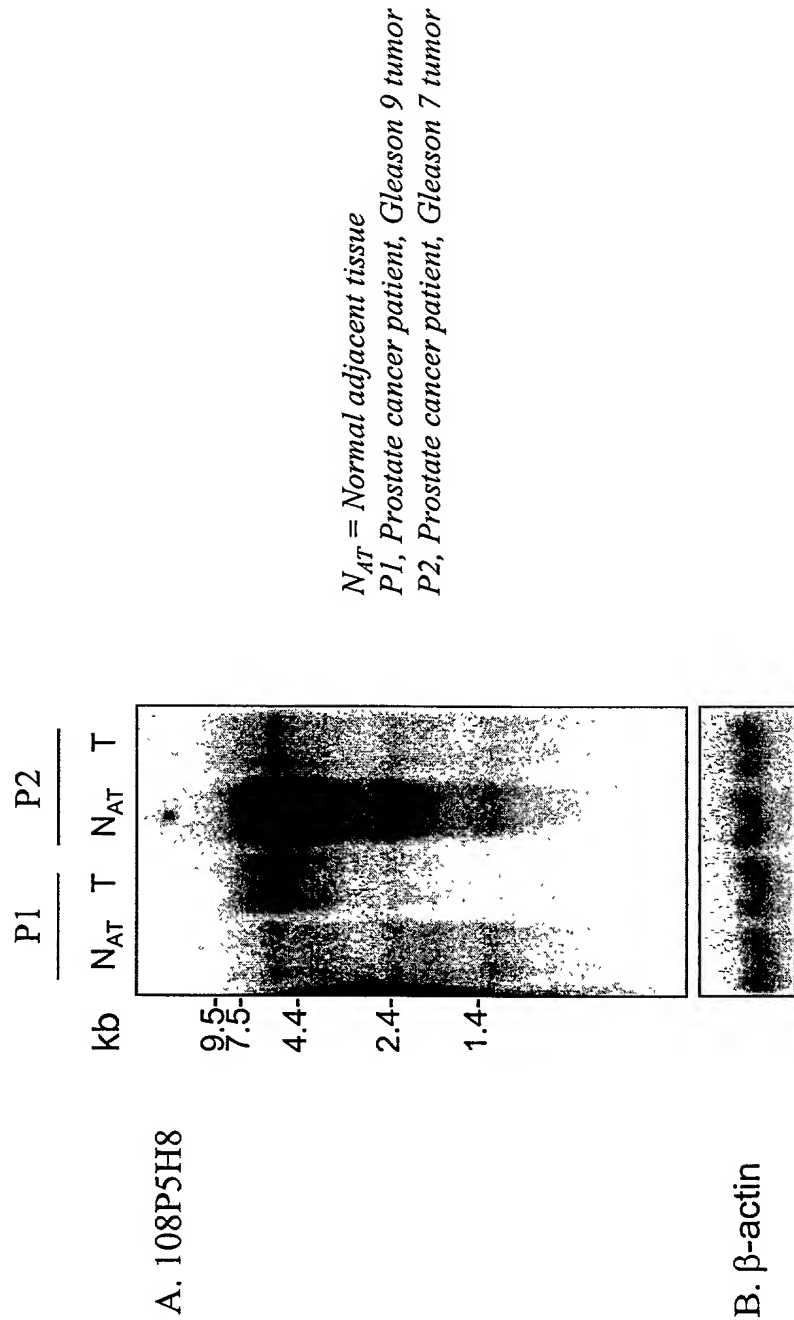


Figure 16 108P5H8 is not Androgen-Regulated

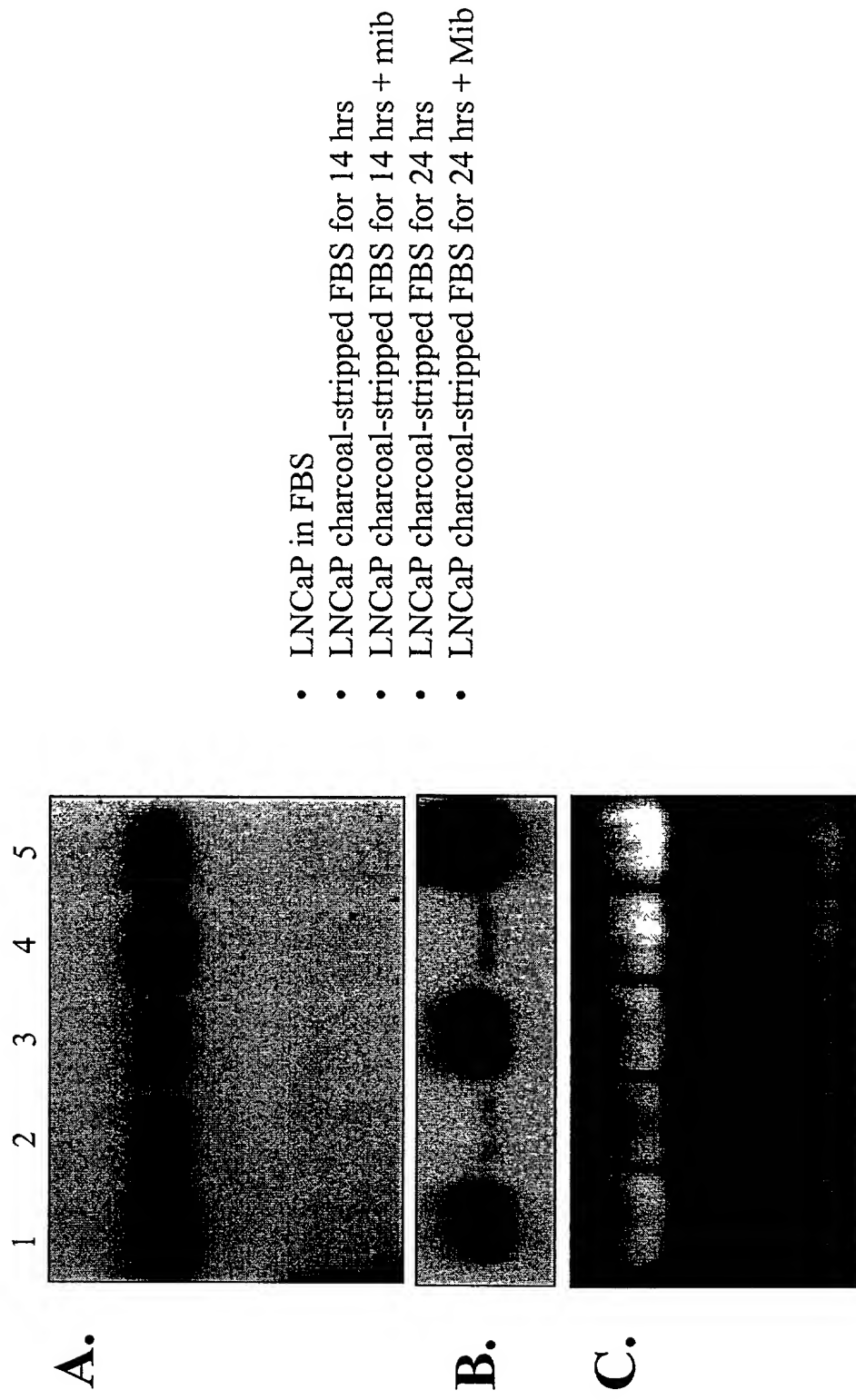
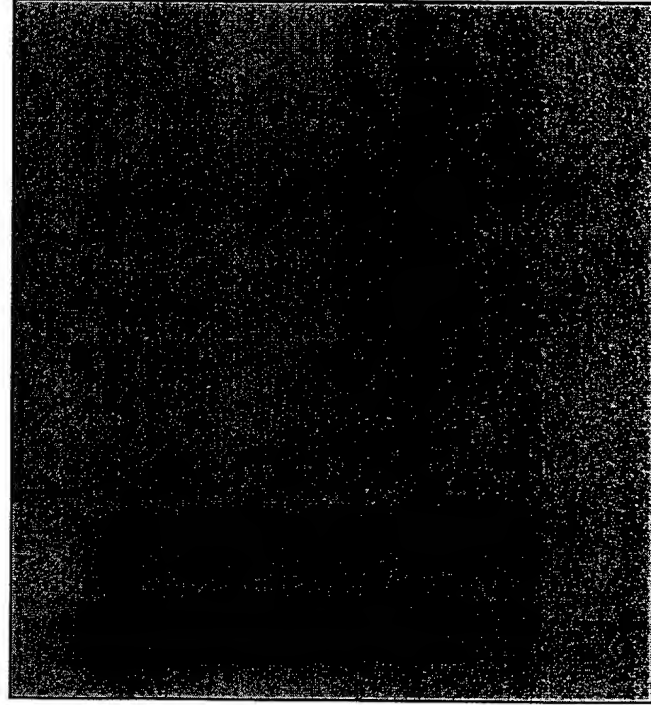


Figure 17 Expression of 108P5H8 in Prostate Cancer Metastasis Specimens

Met1 Met2 NB NK NL NBr NO NPa



*Met1 = Prostate cancer metastasis to lymph
node from patient 1*

*Met2 = Prostate cancer metastasis to lymph
node from patient 2*

NB = normal bladder

NK = normal kidney

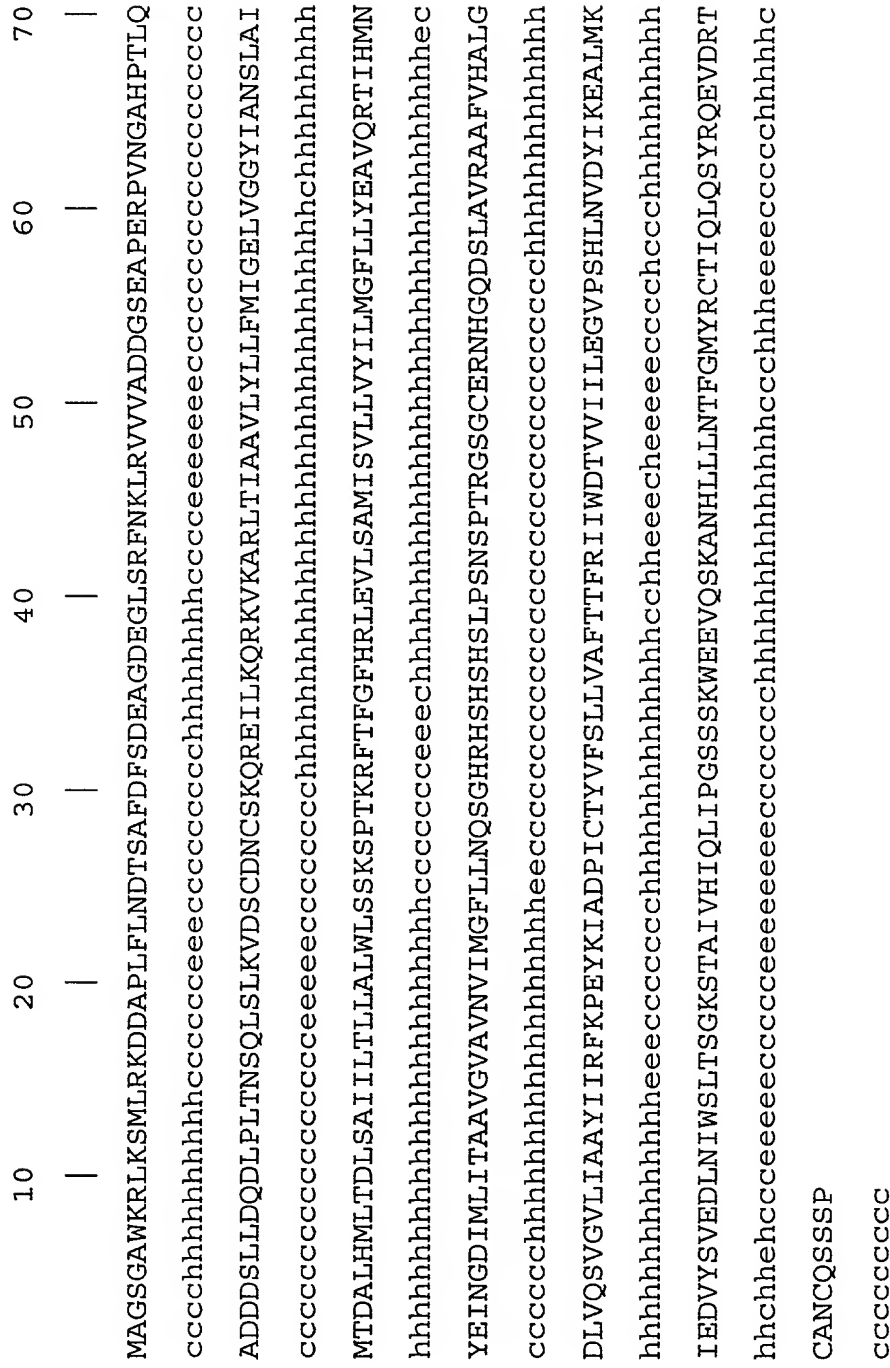
NL = normal lung

NBr = normal breast

NO = normal ovary

NPa = normal pancreas

Figure 18: Secondary structure analysis of 108P5H8



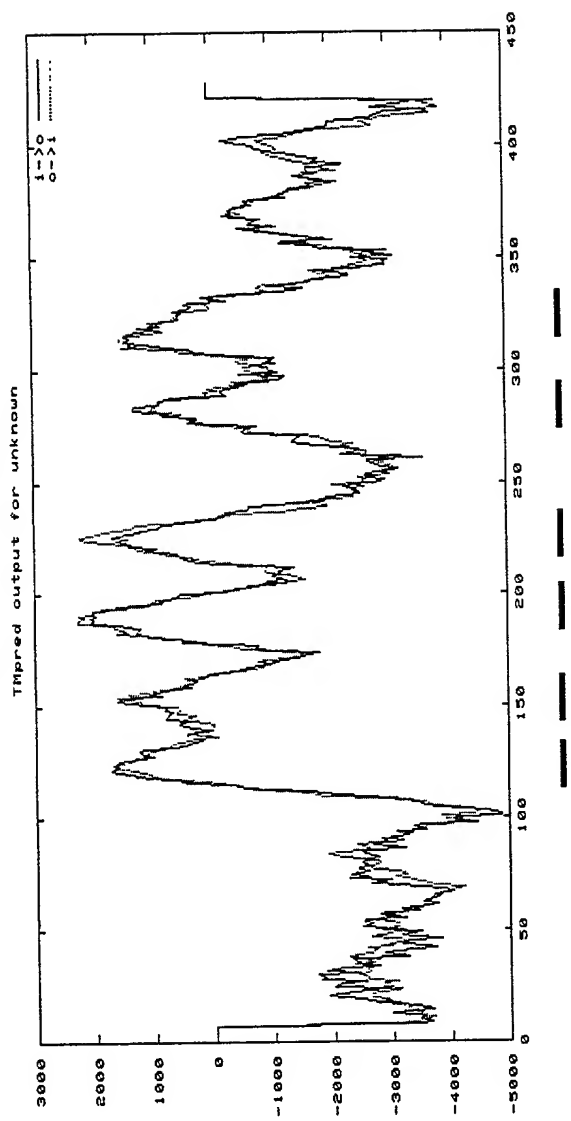
c: random coil (38.46%)
e: extended strand (11.66%)
h: alpha helix (49.88%)

sd-70948

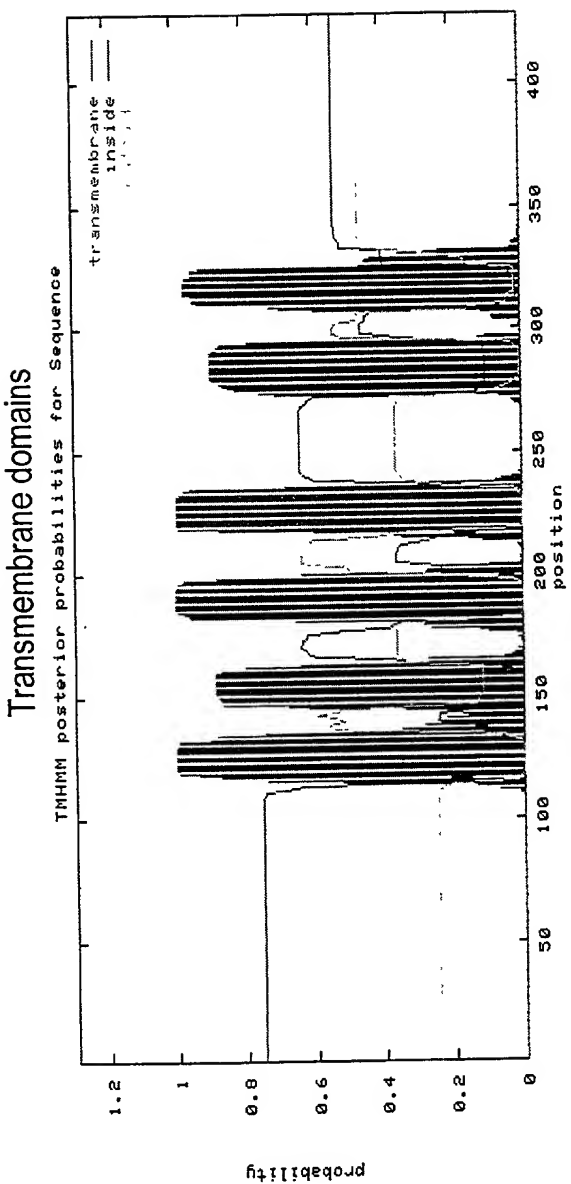
bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Figure 19: Transmembrane region prediction of 108P5H8

A



B



sd-70949

Figure 20: Androgen-independent expression of 108P5H8 in prostate cancer cells

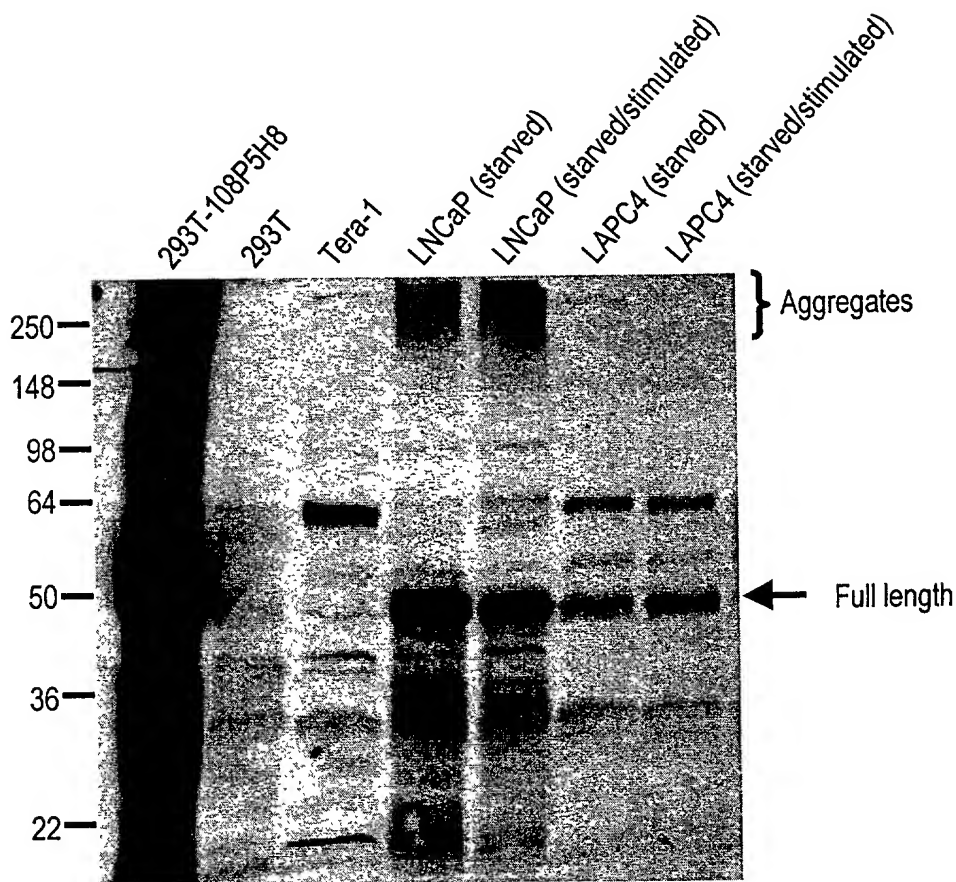


Figure 21: Surface expression of 108P5H8 in prostate cancer cells

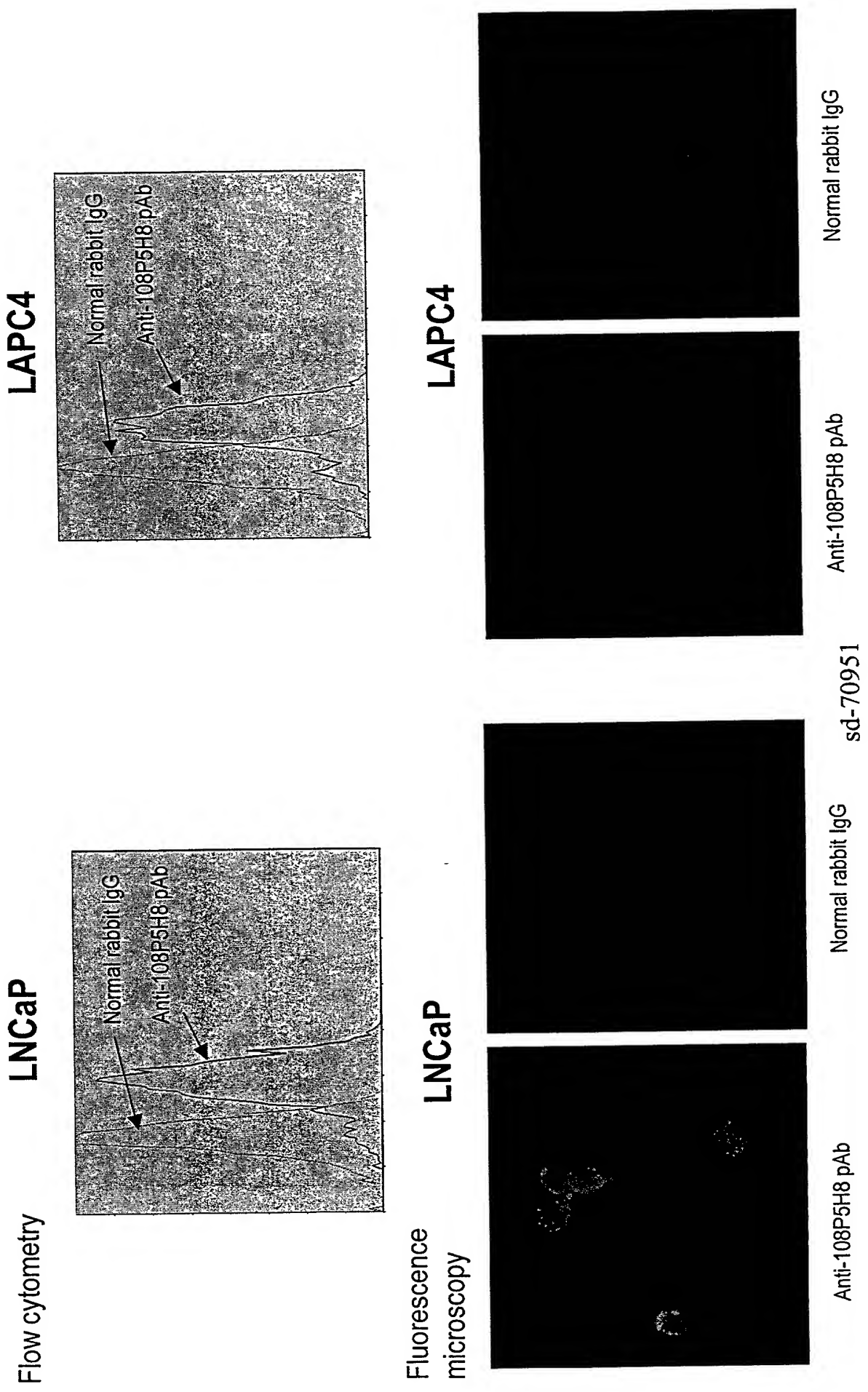
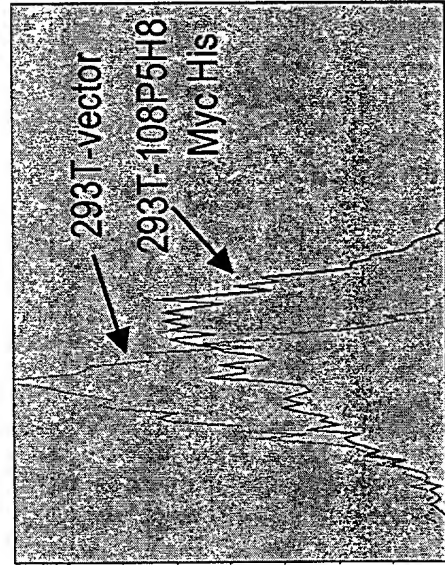


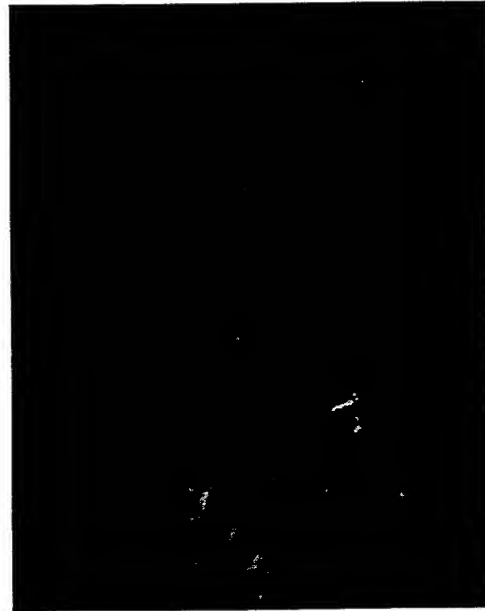
Figure 22: Surface expression of 108P5H8 in 293T cells

Flow cytometry

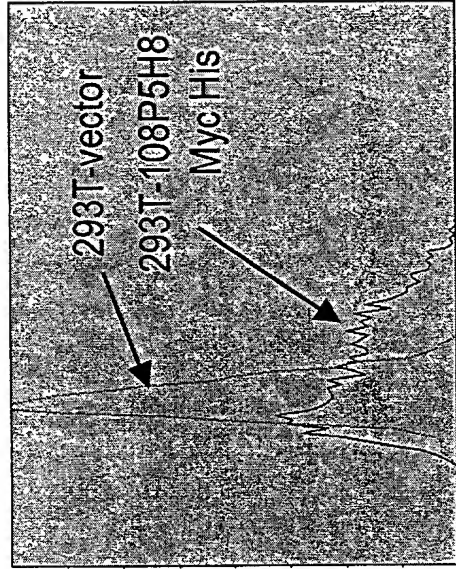


Anti-His pAb

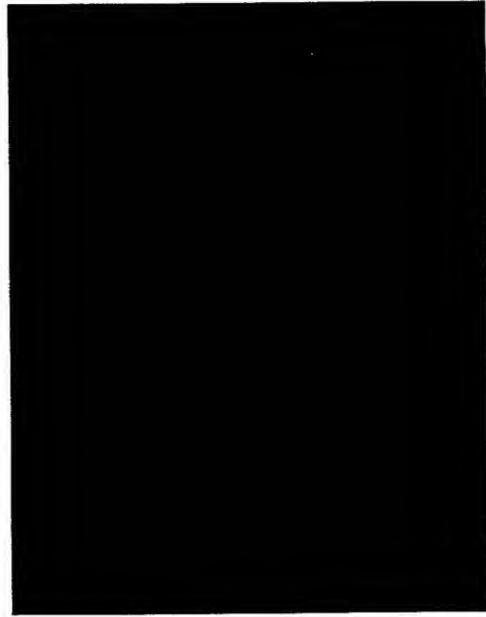
Fluorescence
microscopy



293T-108P5H8



Anti-108P5H8 pAb

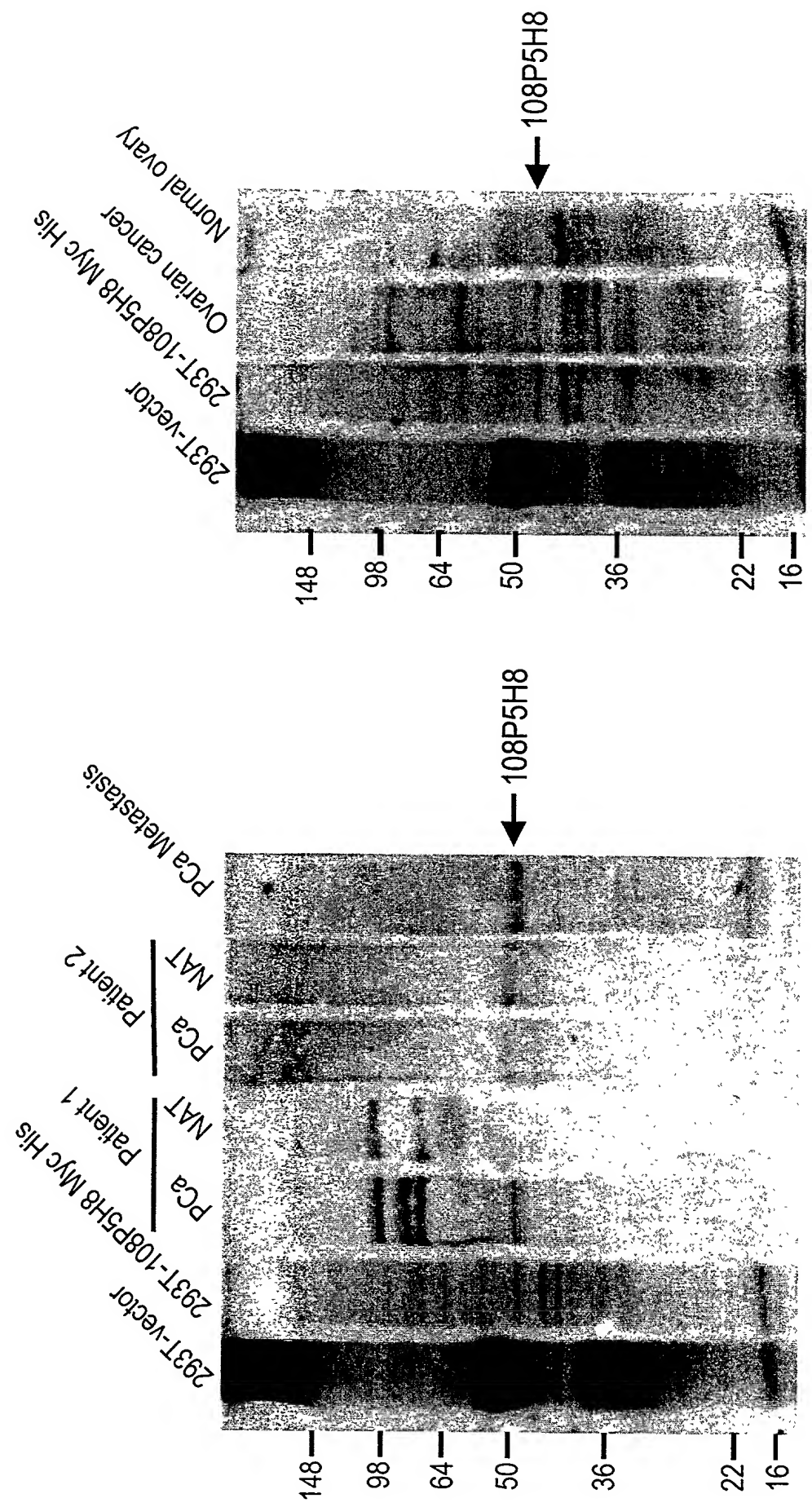


293T-vector

Anti-108P5H8 pAb

bioRxiv preprint doi: <https://doi.org/10.1101/2019.04.11.334444>; this version posted April 11, 2019. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

Figure 23: Expression of 108P5H8 in prostate and ovarian cancer patient specimens



**Figure 24: Expression of 108P5H8
in engineered cell lines**

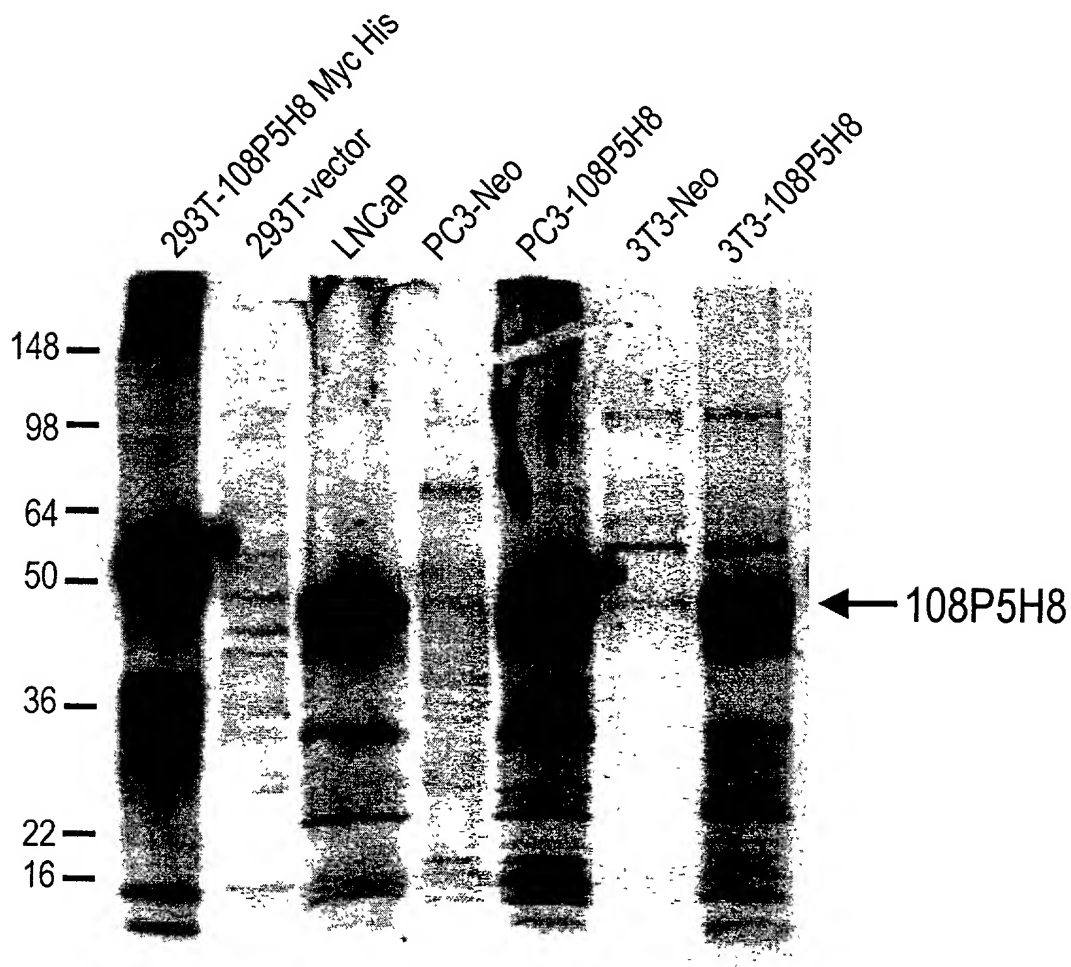


Figure 25: Alignment of 108P5H8 v.1 protein with members of the zinc transporter family.

A-Alignment of 108P5H8 with the human zinc transporter 4, i.e. gi 11432533.

Identities = 429/429 (100%), Positives = 429/429 (100%)

```
108P5: 1  MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
      MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER
Sbjct: 1  MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61  PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCQREILKQRKVKARLTIAAVL 120
      PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCQREILKQRKVKARLTIAAVL
Sbjct: 61  PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCQREILKQRKVKARLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAIILTLALWLSSKSPTKRFTFGFHRLE 180
      YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAIILTLALWLSSKSPTKRFTFGFHRLE
Sbjct: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAIILTLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240
      VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG
Sbjct: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240

108P5: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
      HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE
Sbjct: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
      YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL
Sbjct: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVILLEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420
      NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR
Sbjct: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420

108P5: 421 CANCQSSSP 429
      CANCQSSSP
Sbjct: 421 CANCQSSSP 429
```

B-Alignment of 108P5H8 with the human zinc transporter ZNT4, i.e. gi 8134840

Identities = 428/429 (99%), Positives = 429/429 (99%)

```
108P5: 1  MAGSGAWKRLKSMRLRKDDAPLFLNDTSAFDFSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
      MAGSGAWKRLKSMRLRKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER
Sbjct: 1  MAGSGAWKRLKSMRLRKDDAPLFLNDTSAF+FSDEAGDEGLSRFNKLRVVVADDGSEAPER 60

108P5: 61  PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCQREILKQRKVKARLTIAAVL 120
      PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCQREILKQRKVKARLTIAAVL
Sbjct: 61  PVNGAHPTLQADDDSLLDQDLPLTNSQLSLKVDSCDNCQREILKQRKVKARLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAIILTLALWLSSKSPTKRFTFGFHRLE 180
      YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAIILTLALWLSSKSPTKRFTFGFHRLE
Sbjct: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDLSAIILTLALWLSSKSPTKRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240
      VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG
Sbjct: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQSG 240

108P5: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
      HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE
Sbjct: 241 HRHSHSHSLPSNSPTRGSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFKPE 300
```

108P5: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVEDL 360
YKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVEDL
Sbjct: 301 YKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVEDL 360

108P5: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420
NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR
Sbjct: 361 NIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEVDR 420

108P5: 421 CANCQSSSP 429
CANCQSSSP
Sbjct: 421 CANCQSSSP 429

C-Alignment of 108P5H8 with the rat zinc transporter ZNT-4, i.e. gi 8134837

Identities = 387/430 (90%), Positives = 407/430 (94%), Gaps = 3/430 (0%)

108P5: 1 MAGSGAWKRLKSMRLKDDAPLFLNDTSADFSDSDEAGDEGLSRFNKLRVVVADDGSEAPER 60
MAG GAWKRLKS+LRKDDAPLFLNDTSADF DE DEGLSRFNKLRVVVADD SEAPER
Sbjct: 1 MAGPGAWKRLKSLLRKDDAPLFLNDTSADFDFLDEVSDSDEGLSRFNKLRVVVADDSEAPER 60

108P5: 61 PVNGAHP TLQADDDSLLDQDLPLTNSQLSLKVDSCDNCSKQREILKQRKVKARLTIAAVL 120
PVNGAHP LQADDDSLLDQ+LPLTNSQLSLK+D CDNCSK+RE+LKQRKVK RLTIAAVL
Sbjct: 61 PVNGAHPALQADDDSLLDQELPLTNSQLSLKMDPCDNCSKRRELLKQRKVKTRLTIAAVL 120

108P5: 121 YLLFMIGELVGGYIANS LAIMTDALHMLTDL SAI ILTLLALWLSSKSPTKRFTFGFHRLE 180
YLLFMIGELVGGY+ANSLAIMTDALHMLTDL SAI ILTLLALWLSSKSPT+RFTFGFHRLE
Sbjct: 121 YLLFMIGELVGGYMANSLAIMTDALHMLTDL SAI ILTLLALWLSSKSPTRRFTFGFHRLE 180

108P5: 181 VLSAMISVLLVYILMGFLLYEAVQRTIHMNYEINGDIMLITAAGVAVNVIMGFLLNQ-- 238
VLSAMISV+LVY+LMGFLLYEAVQRTIHMNYEINGD+MLITAAGVAVNVIMGFLLNQ
Sbjct: 181 VLSAMISVMLVYVLMGFLLYEAMQRTIHMNYEINGDVMLITAAGVAVNVIMGFLLNQSG 240

108P5: 239 SGHRHSHSHSLPSNSPTRSGCERNHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 298
H H+HSHSLPSNSP+ S +HGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK
Sbjct: 241 HHHSHAHSHSLPSNSPSMVSS-GHSHGQDSLAVRAAFVHALGDLVQSVGVLIAAYIIRFK 299

108P5: 299 PEYKIADPICTYVFSLLVAFTTFRIIWDTVVIIIEGVPSHLNVDYIKEALMKIEDVYSVE 358
PEYKIADPICTY+FSLLVAFTT RIIWDTVVIIIEGVPSHLNVDYIKE+LMKIEDVYSVE
Sbjct: 300 PEYKIADPICTYIFSLVAFTTLRIIWDTVVIIIEGVPSHLNVDYIKESLMKIEDVYSVE 359

108P5: 359 DLNIWSLTSGKSTAIVHIQLIPGSSSKWEEVQSKANHLLLNFTFGMYRCTIQLQSYRQEV 418
DLNIWSLTSGK+TAIVH+QLIPGSSSKWEEVQSKA HLLLNFTFGMY+CT+QLQSYRQE
Sbjct: 360 DLNIWSLTSGKATAIVHMLIPGSSSKWEEVQSKAKHLLLNFTFGMYKCTVQLQSYRQEAT 419

108P5: 419 RTCANCQSSS 428
RTCANCQSSS
Sbjct: 420 RTCANCQSSS 429

Figure 26: Expression of 108P5H8 in LNCaP cells

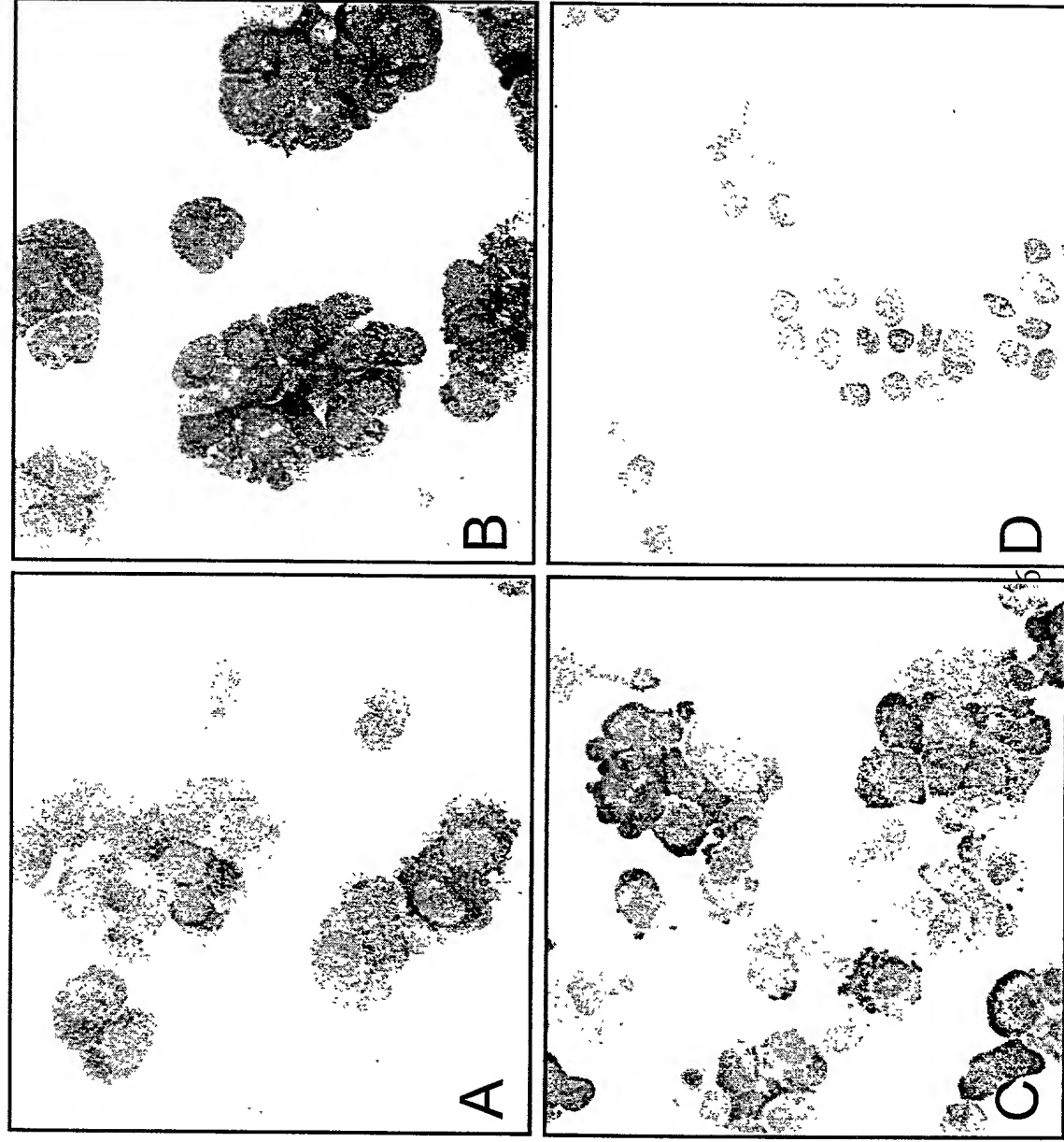
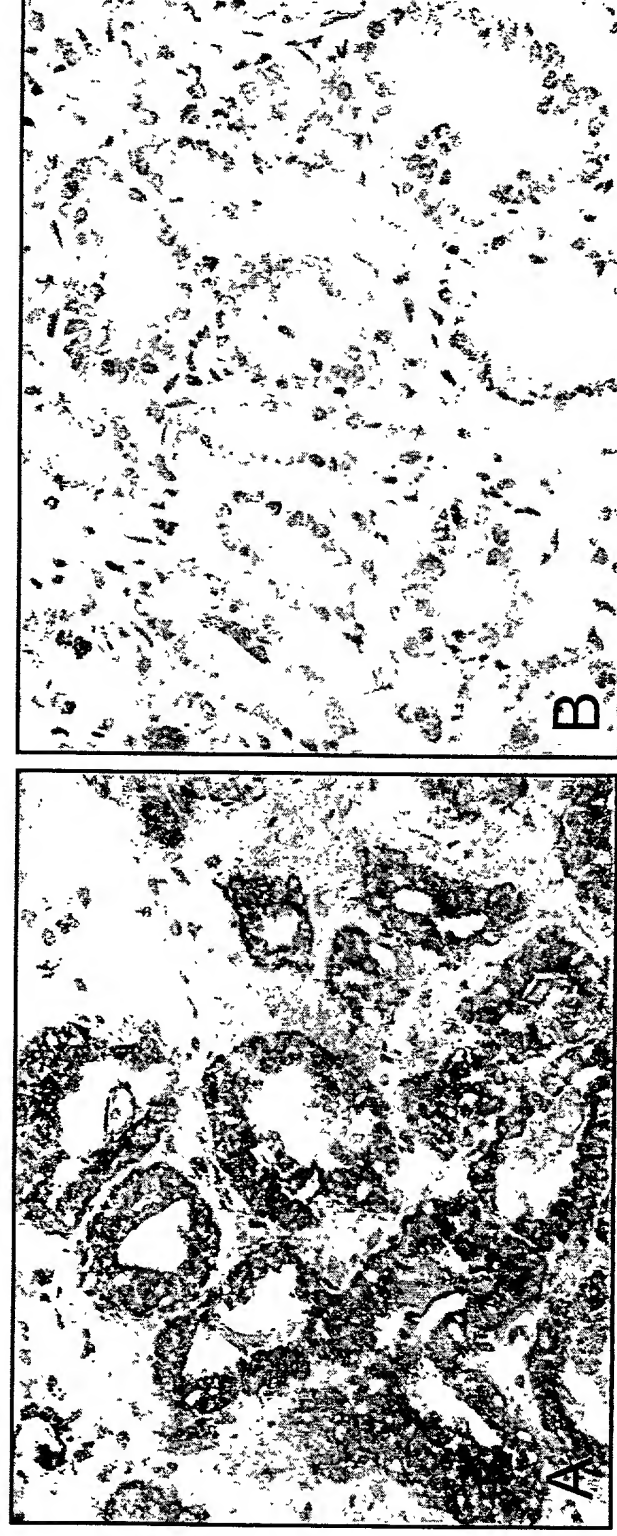
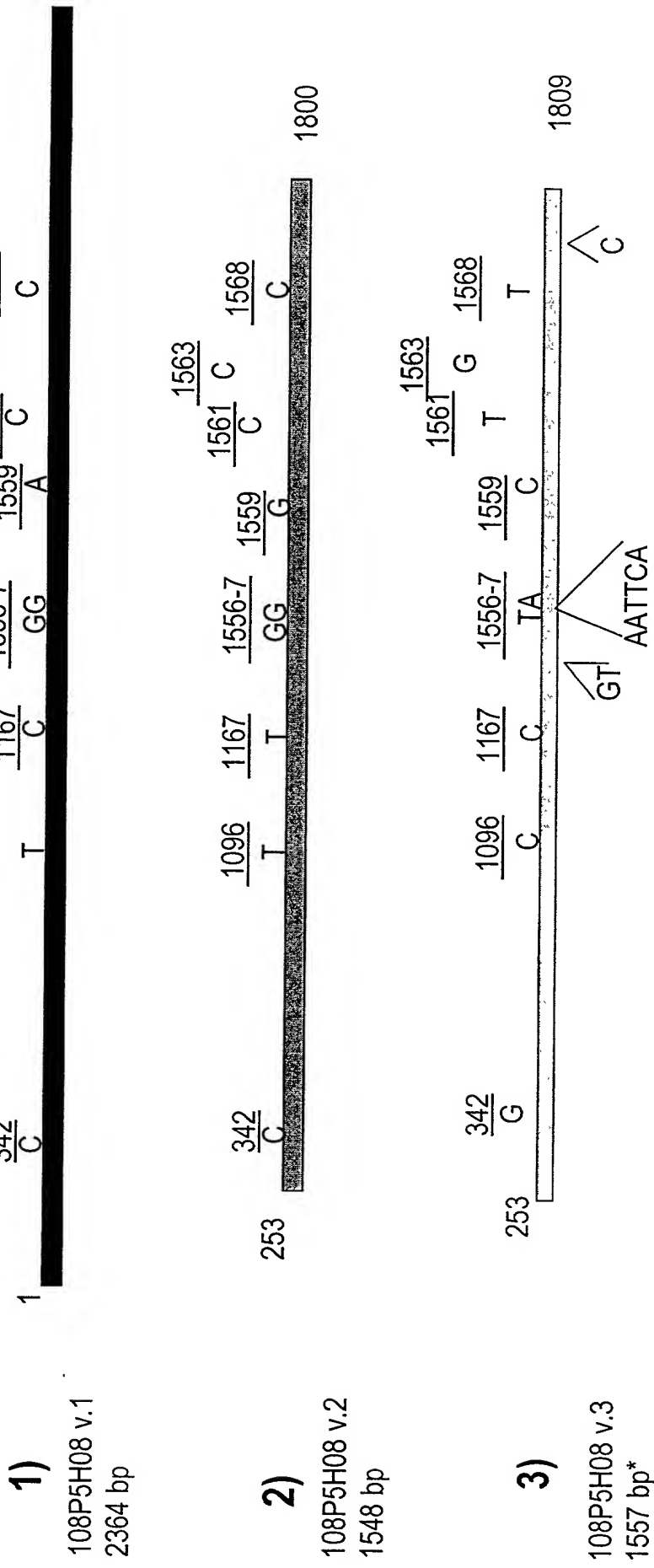


Figure 27:
Expression of 108P5H8 in Prostate Carcinoma
(Gleason grade 6)



sd-70960

Figure 28A



*There are three insertions in variant 3: GT, AATTCA and C at 1553, 1566 and 1784, respectively; numbering is relevant to variant 1.

Figure 28B

30

1)

108P5H08 v.1

429 a. a.

D

1

429



30

2)

108P5H08 v.3

429 a.a.

E

1

429

